

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 15:51:16 : Search time 172.18 Seconds
(without alignments) 471.220 Million cell updates/sec

Title: US-09-052-089a-1
Perfect score: 2384
Sequence: 1 MPRLACTICSDPFHSDRV.....VRKTVPSLQAKLPTFLWS 469

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	ID	Description
1	2384	100.0	469	4	000467
2	2357	98.9	469	4	Q9BWF2
3	1870.5	77.5	470	11	Q9CWP4
4	1847.5	77.5	470	11	Q08854
5	955	40.1	223	13	Q922M8
6	925	38.8	433	13	Q9VGN2
7	291.5	12.2	435	5	Q9SSS5
8	286.5	12.0	435	5	Q9VBD7
9	204.5	8.6	506	10	Q9M143
10	188	7.9	1530	4	Q43241
11	185.5	7.8	1930	13	Q9DGD5
12	182	7.6	425	5	P90990
13	182	7.6	1578	10	Q9AY25
14	181	7.6	1931	13	Q42352
15	181	7.6	1958	5	Q96052
16	180	7.6	1092	13	Q90338

17	179	7.5	477	4	Q9Y577
18	179	7.5	1138	5	Q22276
19	178.5	7.5	764	13	Q91411
20	178	7.5	477	11	Q9WV59
21	177.5	7.4	948	4	Q9UKT7
22	177.5	7.4	1133	5	Q21022
23	177.5	7.4	1305	10	Q9FJ35
24	177.5	7.4	1933	13	Q90337
25	177	7.4	879	13	Q9YHD8
26	176.5	7.4	976	11	Q9SM12
27	176.5	7.4	1156	17	Q28714
28	176	7.4	1156	16	Q66878
29	176	7.4	1939	6	Q9TW61
30	175.5	7.4	1929	13	Q98T06
31	175.5	7.4	2473	11	Q9Q284
32	175	7.3	1690	5	Q44829
33	174.5	7.3	529	4	Q9UP51
34	174.5	7.3	1119	13	P87344
35	174	7.3	671	13	Q9YHD4
36	173.5	7.3	975	13	Q98T05
37	173.5	7.3	1743	5	Q96063
38	173	7.3	437	2	Q9AMC4
39	173	7.3	1120	11	Q9SM11
40	172.5	7.2	708	13	Q9YHD7
41	172.5	7.2	1936	13	Q90YF6
42	172.5	7.2	1938	13	Q91BD7
43	171.5	7.2	592	2	Q91AN1
44	171.5	7.2	1938	6	Q9G3P9
45	171.5	7.2	1999	11	Q63731

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	469 AA.
000467	000467			
AC	000467			
DT	01-JUL-1997 (TREMBlrel. 04, Created)			
DT	01-JUL-1997 (TREMBlrel. 04, Last sequence update)			
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
DE	HTIRIP.			
GN	HTIRIP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
FN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97258620; PubMed=9104814;			
RA	Lee S.Y., Lee S.Y., Choi Y.,			
RT	"TRAF-Interacting protein (TRIP): a novel component of the tumor			
RT	necrosis factor receptor (TNFR) - and CD30-TRAF signaling complexes			
RT	that inhibits TRAF2-mediated NF-kappa activation."			
RL	J. Exp. Med. 185:1275-1285(1997).			
CC	- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
DR	EMBL, U77845; AAB52993.1; -			
DR	InterPro: IPR001841; Znf_Fing.			
DR	Pfam: PF00097; zf-C3HC4; 1.			
DR	SMART: SM00184; RING; 1.			
KW	Zinc-finger.			
SQ	SEQUENCE 469 AA; 53138 MW; 2D54ED04B84ABAE4 CRC64;			

Query Match 100.0%; Score 2384; DB 4; Length 469;
Best local similarity 100.0%; Pred. No. 1.7e-121;
Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPRLACTICSDPFHSDVAHICGHTFHLOCIOSFEFAPSTPCOCRIQVCKRTIIIN 60
Db	1	MPRLACTICSDPFHSDVAHICGHTFHLOCIOSFEFAPSTPCOCRIQVCKRTIIIN 60
Qy	61	KLFPDLAEEENVDREFLKNELNDVRAQLSQDKERKRDQVVIDTFLRDTLEERNATVVS 120

Db 61 KLFDLAEENVDLREFLKNELDNVRAQLSQDKKEKDSQVITDLRDTLEERNATVVS 120
Qy 121 LQQAALGRAEMLCSTLKQMKYLEQOODETKQAQEEAGRLSRMKMTQEIILLQSQLEBEV 180
Db 121 LQQAALGRAEMLCSTLKQMKYLEQOODETKQAQEEAGRLSRMKMTQEIILLQSQLEBEV 180
Qy 181 EEMIRDMGVGSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRLKDLFSSRSKLQTVY 240
Db 181 EEMIRDMGVGSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRLKDLFSSRSKLQTVY 240
Qy 241 SELDOAKLELSAQKDLQDQADKEIMSLKKLTMLQETLNPVASETVDRLVLESAPAVE 300
Db 241 SELDOAKLELSAQKDLQDQADKEIMSLKKLTMLQETLNPVASETVDRLVLESAPAVE 300
Qy 301 VNLKLRPSFRDDIDLNTFPDVPAPPASSQHGYYEKLCEKSHSPIDQVPRKICKGP 360
Db 301 VNLKLRPSFRDDIDLNTFPDVPAPPASSQHGYYEKLCEKSHSPIDQVPRKICKGP 360
Qy 361 RKESQLSLGGOSGAGEPDEELVGAFPIFVRNALIGQOKPKRPRRESSCKDVVTRTGFGL 420
Db 361 RKESQLSLGGOSGAGEPDEELVGAFPIFVRNALIGQOKPKRPRRESSCKDVVTRTGFGL 420
Qy 421 GGRKFTIOPDTVMIRPLPVKPKTKVKQVRVKTVPSLFOAKLDTFLMS 469
Db 421 GGRKFTIOPDTVMIRPLPVKPKTKVKQVRVKTVPSLFOAKLDTFLMS 469

RESULT 2
Q9BMF2 09BMF2 PRELIMINARY; PRT; 469 AA.
AC Q9BMF2;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE TRAF-INTERACTING PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LONG CARCINOMA;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: BC000310; AAHQ001841; Znf_Ting.
DR InterPro: IPR001841; Znf_Ting.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 469 AA; 53294 MW; B9EF3808FB5C5985B CRC64;

Query Match 98.9%; Score 2357; DB 4; Length 469;
Best Local Similarity 99.1%; Pred. No. 4.8e-120;
Matches 465; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPFALCTICSDFFDHSRDVAIHGHTFHLCQLQSFETAPSRPCQCRIOYQKRTIIN 60
Db 1 MPFALCTICSDFFDHSRDVAIHGHTFHLCQLQSFETAPSRPCQCRIOYQKRTIIN 60
Qy 61 KLFDLQAEENVDLREFLKNELDNVRAQLSQDKKEKDSQVITDLRDTLEERNATVVS 120
Db 61 KLFDLQAEENVDLREFLKNELDNVRAQLSQDKKEKDSQVITDLRDTLEERNATVVS 120
Qy 121 LQQAALGRAEMLCSTLKQMKYLEQOODETKQAQEEAGRLSRMKMTQEIILLQSQLEBEV 180
Db 121 LQQAALGRAEMLCSTLKQMKYLEQOODETKQAQEEAGRLSRMKMTQEIILLQSQLEBEV 180
Qy 181 EEMIRDMGVGSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRLKDLFSSRSKLQTVY 240
Db 181 EEMIRDMGVGSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRLKDLFSSRSKLQTVY 240

Qy 241 SELDOAKLELSAQKDLQDQADKEIMSLKKLTMLQETLNPVASETVDRLVLESAPAVE 300
Db 241 SELDOAKLELSAQKDLQDQADKEIMSLKKLTMLQETLNPVASETVDRLVLESAPAVE 300
Qy 301 VNLKLRPSFRDDIDLNTFPDVPAPPASSQHGYYEKLCEKSHSPIDQVPRKICKGP 360
Db 301 VNLKLRPSFRDDIDLNTFPDVPAPPASSQHGYYEKLCEKSHSPIDQVPRKICKGP 360
Qy 361 RKESQLSLGGOSGAGEPDEELVGAFPIFVRNALIGQOKPKRPRRESSCKDVVTRTGFGL 420
Db 361 RKESQLSLGGOSGAGEPDEELVGAFPIFVRNALIGQOKPKRPRRESSCKDVVTRTGFGL 420
Qy 421 GGRKFTIOPDTVMIRPLPVKPKTKVKQVRVKTVPSLFOAKLDTFLMS 469
Db 421 GGRKFTIOPDTVMIRPLPVKPKTKVKQVRVKTVPSLFOAKLDTFLMS 469

RESULT 3
Q9CP4 09CP4 PRELIMINARY; PRT; 470 AA.
AC Q9CP4;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE TRAF-INTERACTING PROTEIN.
GN TRAF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC SFRAIN-C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawaji J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arai K., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Alkawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Salto T., Okazaki Y., Gotohori T., Bono H., Kusunaga T., Salto R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli T., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AK012786; BAB28469.1; -.
DR MGD: MGI:1096377; Trafp.
DR InterPro: IPR001841; Znf_Ting.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 470 AA; 53149 MW; EBFAC49A9F4BF2E CRC64;

Query Match 78.5%; Score 1870.5; DB 11; Length 470;
Best Local Similarity 79.1%; Pred. No. 9.2e-94;
Matches 370; Conservative 42; Mismatches 55; Indels 1; Gaps 1;

Qy 1 MPFALCTICSDFFDHSRDVAIHGHTFHLCQLQSFETAPSRPCQCRIOYQKRTIIN 60
Db 1 MPFALCTICSDFFDHSRDVAIHGHTFHLCQLQSFETAPSRPCQCRIOYQKRTIIN 60

DE TRAF INTERACTING PROTEIN.
 GN TRIP.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
 OC Tetraodontidae; Takifugu.
 NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99148833; PubMed=10025966;
 RA Côté A.J., Clark M., Hawker K., Umranta Y., Wheller D., Bishop M.,
 RA Elgar G.,
 RT "Three receptor genes for plasmalogen related growth factors in the
 RT genome of the puffer fish Fugu rubripes."
 RL FEBS Lett. 443:370-374(1999).
 CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL; AJ010317; CA009084.1; -
 DR InterPro; IPR001841; Znf_1ing.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 DR Zinc-finger
 KW
 SQ SEQUENCE 433 AA; 49201 MW; A8C31AAA4216E8C2 CRC64;

Query Match 38.8%; Score 925; DB 13; Length 433;
 Best Local Similarity 43.8%; Pred. No. 9.8e-43;
 Matches 197; Conservative 76; Mismatches 121; Indels 56; Gaps 5;

QY 1 MPALCTICSDFFDHSRDVAIHGHTFHLQCLIQSFETAPSRTPCPCRIQVGRKTIIN 60
 DB 1 MPAACTICSDFFDHSRDVAIHGHTFHLQCLIQSFETAPSRTPCPCRIQVGRKTIIN 60
 QY 61 KLFDLQAEENVDREFLKNELDNVAQLSQKDEKRSQVITDRLDTEENATVVS 120
 DB 61 KLFDVGLDSSVDPESLQNELDRVAVKVFSSKERDWEKQKAMDLMETVELQKALEN 120
 QY 121 LQALGRAEMLSTLTKKMYLEQODETKQAOEAGRLRSMKMTMEQIELLSQSLPEV 180
 DB 121 LQKVMKEKCKSALRQMTYLEQSHNDTRAKEVRLRKTMTFESLDVYLOGQRAEV 180
 QY 181 EEMIRDMGVGSAVEQLAVYCVSLKKEVENLEKARKASGEVADLRDLFSSRSKLOTYV 240
 DB 181 ESMITDMGIGAAVEQLAVYCVSLKKEVENLEKARKASGEVADLRDLFSSRSKLOTYV 240
 QY 241 SELQAKLELKSADQKLSADKELMSLKKLTMLQETLNPVASEVNDRLVE--SPAP 298
 DB 241 LELTKADMDKSLQNDLNLNKEKISLKKVEFLQELALSTPTRTNEALGRLLFERCGAAP 300
 QY 299 -----VEVNLKLRSPFRDDIDLNATFDVDTPPARPSSSQHGVEKLCLEKSHSPIDVP 353
 DB 301 PONSRAVSKASCLHPPSNGEDIDLMYDVTTP-----DDVR 336
 QY 354 KTKCKGRKESQSLSGQSCAGEPDELVGAFPIEVNAILGOKOPRPNSESSCSKDVV 413
 DB 337 KRPKVPYSKKMHL-----DSVILLRTKYKNLVSNQK-----FV 371
 QY 414 RTGFDGLGGRKFTQPTDVTWIRPLPVKPK 443
 DB 372 QSGTDLGGLGRTKFTQPTTHAVRSEASKPE 401

RESULT 7
 095SS5 PRELIMINARY; PRT; 435 AA.
 AC 095SS5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GH03577P.
 GN CG5140.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Y, CN BW SP;
 RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY060610; AAL28158.1; -
 SQ SEQUENCE 435 AA; 48455 MW; 0BFF0AC91DD9416E CRC64;

Query Match 12.2%; Score 291.5; DB 5; Length 435;
 Best Local Similarity 25.1%; Pred. No. 1.6e-08;
 Matches 113; Conservative 82; Mismatches 161; Indels 95; Gaps 18;

QY 7 CTICSDFFDHSRDVAIHGHTFHLQCLIQSFETAPSRTPCPCRIQVGRKTIIN 66
 DB 6 CVICAEELFGQADVEFAVYCGMFHNLQMDLR--SKTCPCQCKNCKTTRNIF-RVFN 62
 QY 67 AOEENVDREFLKNELDNVAQLSQKDEKRSQVITDRLDTEENATVVS 126
 DB 63 ANDVSHIDVCSLOEODNMLSMKMYEKERNDEQIIRDLKETQKCLTIAGLEKQV 122
 QY 127 KAEMLCSTLTKKMYLEQODETKQAOEAGRLRSMKMTMEQIELLSQSLPEVEIMRD 186
 DB 123 KKDPLISSVYEQIGVLKSDAHVVDGLRKEMKTKLSQISMEGSAIILAASADADRLKN 182
 QY 187 MGVGSAVEQLAVYCVSLKKEVENLEKARKASGEVADLRDLFSSRSKLOTYVS 242
 DB 183 -----EADPHVLANVSTLTKELROCESKKTLELRNVAVYONDLEKTELK-KLEERVSH 237
 QY 243 LD-----QAKL---ELKSADKLSA---DKELMSLKKLTMLQETLNPVASETVYD 289
 DB 238 LESDLYAOEKLQAFKFKTAYLDSPNASCGLNSIILAKNE---EKRTTISPVKENIK 293
 QY 290 RLYESPAPVPEVNLKLRSPFRDDIDLNATFDVDTPPARPSSSQHGVE-----KICLE 343
 DB 294 R-IEESTSPY-LNIK-----SSSVGLAHLNLTGNIGLA 325
 QY 344 KSH-SPIQDVPKIKCKPRKESQSLSGQSCAG---EPDEELVGAPPIVNAAILGOK 398
 DB 326 KSKTSPKIGV-----GVSKTSTIRKTSDDSEKYSIF-----K 362
 QY 399 PKRPSSESCSKDVVRG---FDGLGGRK 425
 DB 363 PRLLGSSSSSALATGTSNPNVYMGMSSEK 393

RESULT 8
 09VBD7 PRELIMINARY; PRT; 455 AA.
 AC 09VBD7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CG5140 PROTEIN.
 GN CG5140.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,


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0y 364 -----SGLSLGGCGCAEPEDELVGAPFIVRNALIGQKPKPRRSSGCKVVR 414
Db 407 SGNIMSSGTTNIRGRMSKHEERNE---ATP-----SLGGSVPRK-----DDLIS 448
Oy 415 TGFDLGGRTKFIQ 428
   | | | | |
Db 449 IGPDKGGRKIVLR 462

RESULT 10
043241
ID 043241 PRELIMINARY; PRT: 1530 AA.
AC 043241;
DT 01-JUN-1998 (TREMBLrel, 06, Created)
DT 01-JUN-1998 (TREMBLrel, 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel, 19, Last annotation update)
DE GCP170..
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97442456; PubMed=9295333;
RA Misumi Y., Sohma M., Yano A., Fujiwara T., Ikehara Y.;
RT "Molecular Characterization of GCP170, a 170-kDa Protein Associated
   with the Cytoplasmic Face of the Golgi Membrane."
RL J. Biol. Chem. 272:23851-23858(1997).
SQ EMBL: D63397; BAA23661.1; -.
DQ SEQUENCE 1530 AA; 170268 MW; E3851F2ABFA1A533 CRC64;

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AC 042352;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinus.
NC NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FAST MUSCLE;
RX MEDLINE=9735253; PubMed=9208928;
RA Hirayama Y., Watabe S.;
RT "Structural differences in the crossbridge head of temperature-
RT associated myosin subfragment-1 isoforms from carp fast skeletal
RT muscle."
RL Eur. J. Biochem. 246:380-387(1997).
DR EMBL; D89991; BAA22068.1; -.
DR HSSP; P13538; 2MYS.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001609; myosin_head.
DR InterPro; IPR004009; Myosin_N.
DR InterPro; IPR002928; Myosin_tail.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF02736; Myosin_N; 1.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
SQ SEQUENCE 1931 AA; 221162 MW; 59466B7BD0872DDD CRC64;

Query Match 7.6%; Score 181; DB 13; Length 1931;
Best Local Similarity 21.2%; Pred. No. 0.075;
Matches 92; Conservative 80; Mismatches 163; Indels 98; Gaps 16;

QY 31 LQCLISFETAPSRCTQCRCRQVGGKRTITINKLPFDLAQEEENVLDREF----- 78
DB 1141 LEEISEERLEAGAGATAQIEENKKREADFQKMRDL---EESTLQHEATAAALKKQADT 1197
QY 79 ---LKNLDVNVRAQLSQDKCKRDSQVITDRLRPTLEERNATVVSLOQALGKAMLSTL 135
DB 1198 VAEIGEDIDNQRKQKLEKEKSEYKMEIDDLISNME-----AVAKAGNLEKMCRTL 1250
QY 136 KQMKVLEQOQDETQAOEEAGRLRSKMT-----MEQIELLLOSQLP----- 178
DB 1251 EDQISEIKAKSDENSRLNMNQRARLQTEENGFSRQLEKEALV-SQLTRGQAFITQ 1309
QY 179 -----EVEEMIRDMVGQSAVEQLAVYCVSLKKEYENLKEARKASEVADKLKDLFSS 232
DB 1310 IEDLQRHVEEVEVAKNALAVOSARHDCDLREQYEEEOEAKTEIQRGSKANSEVAQV 1369
QY 233 RSKLQI---VSELDQAKLELKSQDKLOSADKEIMSLKKKILMIOETNLPPVASETV 288
DB 1370 RAYETDAIQRTELEELAKKRL-AQR-LQDAEESIEAVSSKASLETKQ--RLQGEVE 1424
QY 289 DRLV-LESPAPVEVNLKLRPSFRDDI-----DLNKTFFDVDPAPPSQ----- 333
DB 1425 DLWIDGRANAALANLDKQRNF-DKVLAMKQKYESSQALEAKQKAEASLSLELPMK 1483
QY 334 HGYYEKI---CLEKSGSPIQ-----DVPKTKCKPRRSQSLG 369
DB 1484 NSYEALDHLFETLKREKNKLQOEISDLSQELGTGKSHLEKAKKIVSEKAEIQALE 1543
QY 370 GQSGAGEPDEELV 382
DB 1544 EAESTLEHESKI 1556
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RESULT 15
ID 096062 PRELIMINARY; PRT: 1958 AA.
AC 096062;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
CN DMMHC-A.
OS Dugesia japonica (Planarian).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Dugesia.
NC NCBI_TaxID=6161;
RN [1]
RP SEQUENCE FROM N.A.
RA Kobayashi C., Kobayashi S., Oril H., Agata K., Watanabe K.;
RT "Identification of two distinct muscles in the planarian, Dugesia
RT japonica, by the expression of myosin heavy chain genes."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB015484; BAA34954.1; -.
DR HSSP; P24733; 1WDC.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR001637; GlnA_adenyln.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001609; myosin_head.
DR InterPro; IPR004009; Myosin_N.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00612; IQ; 2.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF02736; Myosin_N; 1.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR PRINTS; PR00194; TROPOMYOSIN.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00182; GLN_AADENYLATION; UNKNOWN_1.
DR PROSITE; PS50096; IQ; 1.
SQ SEQUENCE 1958 AA; 224857 MW; 3FE254327DF89524 CRC64;

Query Match 7.6%; Score 181; DB 5; Length 1958;
Best Local Similarity 21.9%; Pred. No. 0.077;
Matches 66; Conservative 66; Mismatches 106; Indels 64; Gaps 9;

QY 60 NKLFDLAQEEENVLDREFLKNELDNVRAQLSQDKCKRDS-----QVIIDTLR 108
DB 878 NDLFLQIQETQDSDLADAEKVSKLVMQKADMESRIKLEEDHLLBEEDASAGLEBMKKMQ 937
QY 109 DTLERNATVVSLOQALGKEMILCSITLKKQMKVLEQOQDETQAOEEAGRLRSKMTMEQ 168
DB 938 GEIEBELKDDVVDLESSLQKAEOKETAKDOQIKAL---QDQIAQEEEMNMKKKEKKADE 994
QY 169 IELLQSQLEPEVEMITDMGVQSAVEQLAVYCVSLKKEYENLKEARKASEVADKLKRD 228
DB 995 LQKTEESLQAEKKAANLKKAKAKLEQ-----TIDEMENLSRQKVADY-EKVKR 1047
QY 229 LFSRSKLIQTVYSELDAQLE---LKSQDKLOSQ-----DKELMSLKK 270
DB 1048 IFEELKQIQETVDDLEVKRELQELKREKMELSNMSKTEDSGVLAQKIKELQAR 1107
QY 271 LTMQIETL-----NLPPVASETVDRVLE---SPAPVEV-----LKL 305
DB 1108 IOELEEDLEAEQARAKAEKSRHQLGELEELSDRLEEQGATSAQELKMKREAEELKL 1167
QY 306 RR 307
DB 1168 KR 1169

RESULT 16
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090338
ID 090338 PRELIMINARY; PRT: 1092 AA.
AC 090338;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN (FRAGMENT).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinus.
OX NCBI_TaxID=962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FAST MUSCLE;
RX MEDLINE=97176447; PubMed=9023993;
RA Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.;
RT "CDNA cloning of myosin heavy chain isoforms from carp fast skeletal
muscle and their gene expression associated with temperature
acclimation.";
RT J. Exp. Biol. 200:27-34(1997).
RL EMBL: D50475; BAA09068.1; -;
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00194; TROPOMYOSIN.
FT NON TER 1
SQ SEQUENCE 1092 AA; 125885 MW; B6BABA3963BEBA CRC64;

Query Match 7.6%; Score 180; DB 13; Length 1092;
Best Local Similarity 23.5%; Pred. No. 0.046;
Matches 68; Conservative 57; Mismatches 108; Indels 56; Gaps 9;

QY 31 LQCLISFETAPSTCQCRCRQVCKRTINKLFEDLQAEENVVDREF----- 78
DB 302 LEEISELEEREGATAOIEKMKREADFOKMRDL--EESTLQHEXTAALRKQOAT 358
QY 79 ---LKNELDVRAQLSOKDEKRDQSVYIDTLRDLERNAVTVSLOALGKAMLCSTL 135
DB 359 VAEIGEIDNLQRYKQKLEKSEYKMEIDLTSMNE-----AVAKAKGNLEKMCRTL 411
QY 136 KKQKYLEQOODETKQAOEAGRLRSKWT-----MEQIELLSQLP----- 178
DB 412 EDQLSEIKAKSDENSRQLNDWNAQRARLQTFNGEFNRQLEKALV--SQLRGQAFTQ 470
QY 179 -----EVEEKIRDMGVGSQSAVEQLAVYCVSLKREYENLKARKASGEVADKLKDLFSS 232
DB 471 IEDLQRRHVEEVRKKNALAHAVOSARHDCDLRLRQYEEDQAKTELORGMSKANSEVAQW 530
QY 233 RSKLQIQT---VYSELDAQKLELKSQKDLQSGADKEIMSLKKLMLQET 277
DB 531 RAKETDAIQRTLELEFAKKKL--AQR-LQDAEESIEAVSSKASLEKT 576

RESULT 17

QY577
ID 09Y577 PRELIMINARY; PRT: 477 AA.
AC 09Y577;

DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE RING FINGER PROTEIN TERF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Carnivora; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=99011410; PubMed=9792805;
RA Ogawa S., Goto W., Oriimo A., Hosoi T., Ouchi Y., Muramatsu M.,
Inoue S.;

RT "Molecular cloning of a novel RING finger-B box-coiled coil (RBCC)
RT protein, terf, expressed in the testis.";
RL Biochem. Biophys. Res. Commun. 251:515-519(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Ogawa S., Goto W., Oriimo A., Hosoi T., Ouchi Y., Muramatsu M.,
Inoue S.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -/- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF156271; AAD40286.1; -;
DR InterPro: IPR001870; Gamma_carboxylase.
DR InterPro: IPR003877; SPRY.
DR InterPro: IPR003878; SPRY_domain.
DR InterPro: IPR000315; Znf_box.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00622; SPRY; 1.
DR Pfam: PF00643; Zf-B_box; 1.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR PRINTS: PR01406; BBOXZNFINGER.
DR SMART: SM00336; BBOX; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00449; SPRY; 1.
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
KW Zinc_finger.
SQ SEQUENCE 477 AA; 54418 MW; ECA4010661ADD28A CRC64;

Query Match 7.5%; Score 179; DB 4; Length 477;
Best Local Similarity 25.3%; Pred. No. 0.021;
Matches 84; Conservative 56; Mismatches 132; Indels 60; Gaps 14;

QY 5 ALCTGSEFPHSDVAIAHGHFTFHLOCLQSFETAPSR-----TGPCRCRYGV 54
DB 14 ATCSICLDYF---TDPVWTTGHNFCRCACIQLSWEKAGKGRKRGSPCPCEKRENSP 70
QY 55 KRITII-NKLFEDLAQ--EENVDLREFLNELDVRAQLSOKDEKRDQSVYIDTLRDTL 111
DB 71 QRNLPLRNLTKVAMQOHGGLQKODLQCEHNEPLKFCQKDDSP-----ICVVCESR 125
QY 112 EERNATVVSLOALGKAMLCSTLKKQKYLEQOODET--KQAOEAGRLRSKWTMEQI 169
DB 126 EHRHLRVLPAEEAVQGYKL--KLEEDMEYLRQITRTGNLQAREEOSLAEMQCKVERR 182
QY 170 ELLLOSLPEVEEMIRDMGVGSQSAVEQLAVYCVSLKREYENLKARKASGEVADKLKDL 229
DB 183 ERIVLE-----PEKKNLYLV--EEQRLQLALEEBEETASRLRSV 222
QY 230 FSSRSKLQTVYSELDAQKLELKSQKDLQSGAD--KEIMSLKKLMLQETLNLPPVASET 287
DB 223 ACLDRQGHSL--ELLLLQLEERSQGPLQMDKKEPLSRKNV-----SVQCEVAPPT 275
QY 288 VDRLVLESPAVEYNLKIRPSFRDIDLNAT 319
DB 276 RPRTVCRVPGQIEV--LR--GFLEDDVVPDAT 302

RESULT 18

Q22276
ID 022276 PRELIMINARY; PRT: 1138 AA.
AC 022276; Q22276;

DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE T07C4.10 PROTEIN.
GN T07C4.10.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Buck D., Berks M.;

DR SMART; SM00184; RING; 1.
 DR SMART; SM00449; SPRY; 1.
 DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
 KM Zinc-finger
 SQ SEQUENCE 477 AA; 54954 MW; 1AAB42BB02615ADF CRC64;

Query Match 7.5%; Score 178; DB 11; Length 477;
 Best Local Similarity 25.8%; Pred. No. 0.024;
 Matches 86; Conservative 61; Mismatches 114; Indels 72; Gaps 18;

QY 5 ALCTICDFDHSRDVAIHCGHTFHLQCLIQSFETAPSR-----TCPCQRIQVG 54
 DB 14 ATCSICLDYF---TDPAWTAAGHNFCECQIQMSWEKGGKGGKKGGKGGSPCEPCREMS 70
 QY 55 KRIT-INKLF---FDLAQEEENVLDREFLKNELDNVRAQLSQDKKE---KRDQVITDTL 107
 DB 71 QRNLPRRLTLTKVAEMARHGPGLHKRDL-----CQIHQEFLLKFCDDQDPICVVC 121
 QY 108 RDTLEERNATVVSLOQALGKAEMLCSTLKKOMKYL--EQODETKQAQEEAGRLRSKMT 165
 DB 122 REAOEHMHRVLPDEAREKTL--RLBEDIKYLRREMKETTLQAKKEOTLTMOERV 178
 QY 166 MEQIELLQSQLPVEEEMIRDMVGOSAVQCLAVYCVSLKKEYENLKEARKAGEVADKL 225
 DB 179 KERERILE---EFQKVLFLEF-----VEBERRLQILKKEED-----DTL 215
 QY 226 RKDLFSSRSKIQTYSELDAQLEL--KSAOKDLQSD--KEINSLKKLTMLQETLNL 281
 DB 216 GK-LQDSKASLDHQSRSLDILLQLEBOTQOEPLQMDVKTDLTKRESLMQYPEVVL- 273
 QY 282 PVASETVRLVLESPAPVEVNLKLRPSFRDID 314
 DB 274 PVAKTYCRV---PGQIEV-LK---SFQEDV 297

RESULT 21
 ID 09UIK7 PRELIMINARY; PRT; 948 AA.
 AC 09UIK7;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ELKS.
 GN ELKS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nakata T.
 RT "Fusion of a Novel Gene, ELKS, to c-ret in a Papillary Thyroid Carcinoma."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB015617; BAA8763.1; -
 DR InterPro: IPR002017; Spectrin.
 SQ SEQUENCE 948 AA; 108792 MW; 344297FDFC9F7602 CRC64;

Query Match 7.4%; Score 177.5; DB 4; Length 948;
 Best Local Similarity 20.3%; Pred. No. 0.054;
 Matches 83; Conservative 80; Mismatches 135; Indels 111; Gaps 14;

QY 8 TICDFDHSRDVAIHCGHTFHLQCLIQSFETAPSR-----KRTTI 59
 DB 463 TLTNQFSDSKO-----HIEVLKESL-TAKEQRAALQTEVALRLLEKETML 510
 QY 60 N---KLFEDLAQEE-----ENVLDRE-----FLKNDLVNVRQLSQDKKEKRSQ 101
 DB 511 NKTKKQIODNAEKGTOAGETHDKMDVAKERKVVNVQLQKTEINQLEQDLRDKERQMSL 570
 QY 102 VIIDLRLDLEERNATVVSLOQALGKAEMLCSTLKKOMKYLEQOODETKQAQEEAGRL 161

DB 571 ERVKSLOADPTNTDIALTLLEALAEKERITERLK-----EQRDBEREKQGEINDYKK 624
 QY 162 KMTMEQIELLQSQLPVEEEMIRDMVGOS-----AVEQLAVCV- 202
 DB 625 DLKDLKEKVSILQDSEKASLIDLKEHASSLASSGLKDKDSRLKTLLEIQKKEECLK 684
 QY 203 ---SLKKEYENLKEARKAGEVADK---LRKDLFSSRSKIQTYSELDAQLELKSQKD 256
 DB 685 MESQLKAHEALAEAR-ASPMSDRIOHLERETIRKQDESSKQAEVDRLETLKEVENE 743
 QY 257 LQSDAKKEIMSL-----KKRLTMLQETLNLPPVASETVDR 290
 DB 744 KNDKDKIALESLTSNQVADQKKVANKLHKQGEVKKKSAQMLEARREDNLDNDSQ 803
 QY 291 LVLESPAPVEVNLKLRPSFRDIDLNATPDVTPPARPSSQHGYYEK 339
 DB 804 LOVE-----ELLMAMEK-----VKQELSMKAKLSSTOOSLAEK 837

RESULT 22
 ID 021022 PRELIMINARY; PRT; 1133 AA.
 AC 021022; Q21071;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE F59A2.6 PROTEIN.
 GN F59A2.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lightning J.
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z34801; CAA84332.1; -
 DR EMBL; Z66514; CAA84332.1; JOINED.
 DR EMBL; Z66514; CAA91344.1; -
 DR EMBL; Z34801; CAA91344.1; JOINED.
 DR InterPro: IPR000237; GRIP.
 DR Pfam: PF01465; GRIP; 1.
 SQ SEQUENCE 1133 AA; 129239 MW; 92015E790A9DE01F CRC64;

Query Match 7.4%; Score 177.5; DB 5; Length 1133;
 Best Local Similarity 20.5%; Pred. No. 0.066;
 Matches 102; Conservative 103; Mismatches 169; Indels 123; Gaps 22;

QY 46 CPCQRIQVG---RTINKLFPDLAEEENV-----LDREFLKNELDNVRAQ 89
 DB 57 CDALQAEVNEKALREBIQAKYDVDTQKARIQGELEESKVVLESEQAENEQERE 116
 QY 90 LSKDKERKDS-QVIIDRLDRLTEERNATVVS-----LQOALGKAEMLCSTLKKOMY 141
 DB 117 QLAAMEKINSQNIIDVYIKKLEQSEBEVLAAGAIOELTEKLESEKETSTAKTLEA 176
 QY 142 LEQOODETKQAQEEAGRLRSKMTM-----EQTELLQSQLPVEEEMIRDMVGQ- 191
 DB 177 VSKLIDSEETSLKFEFSDMIEMKIQLINCEKQDEAVELLKO-KLEBEVKMMSDVEYOK 235
 QY 192 ---SAYBQLAVYCVSLKKEYENLKEARKAGEVADKLKRLPSRSKIQTY- 240
 DB 236 LLESTSEMKQHAEAIEYKQ---LEEQSS---TENLKAENERN-LKTALLESDE 287
 QY 241 -SELDQAKLELSAQKDLQSDAKKEIMSLKRTLMQET-----LNLPPV 283
 DB 288 SSALSELTKQMAKAKKLELASEKESLREGMDRLQVHNAGQDIDKLOKTWLEMAKI 347
 QY 284 ASETVDRLVLESPAPVEVNLKLRPSFRDIDLNATPDVTPPARPSSQHGYYEKL 343
 DB 348 AKSTEDE-----KLAREQLAGLEL-NAKEDL-----KVVEE 377


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Db 1311 IEDLKRVEEVEVAKNALAHAYOSARHDCDLLRQYEEBEAKAELORGMSKANSEVAQM 1370
QY 233 RSKLOT-----VYSELDQAKLELSAQKDLQADKEITSLKKLTLMQETLNPVASETV 288
Db 1371 RAKYETDAIORTTELEESKKKL--AQR-LQDAEESIEAVNSKCSLEKTKRQ--RIQSEVE 1425
QY 289 DRLV-LESPAPVEVNLKRRPSF 310
Db 1426 DLMIDGERANALANLDDKKORNF 1448

RESULT 25
Q9YHD8 PRELIMINARY; PRT: 879 AA.
AC Q9YHD8;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE MYOSIN HEAVY CHAIN (FRAGMENT).
GN MHC-1.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxId=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TAIL MUSCLE; HINDLIMB MUSCLE;
RA Hu H., Merrifield P., Atkinson B.G.;
RT "Expression of the Myosin Heavy Chain Genes in the Tail Muscle of
RT Thyroid Hormone-Induced Metamorphosing Rana catesbeiana Tadpoles.";
RL Dev. Genet. 0:0-0(1999).
DR EMBL: AF097904; ADL3769.1; -
DR InterPro: IPR002928; Myosin_tail.
DR Pfam: PF01576; Myosin_tail.1.
DR PRINTS: PR00194; TROPOMYOSIN.
FT NON TER 1
SQ SEQUENCE 879 AA; 101710 MW; 1C456851E968A3D8 CRC64;

Query Match 7.4%; Score 177; DB 13; Length 879;
Best Local Similarity 22.8%; Pred. No. 0.053;
Matches 107; Conservative 82; Mismatches 184; Indels 96; Gaps 19;

QY 45 TPCPCRIQVGRKTIINKLFDLQAEENVL-----DREFLKNELDNVRAQLSQKDKK-- 97
Db 214 TAQRARLQTENGELSRQL-----EKEESLITQLSRGQAFQCTYELRLQLEETKAKNA 268
QY 98 -----RDSOYLIDFLRQTLERNAIVVSLQALGKAE-----MCSITLK 137
Db 269 LAHALQSSRRHCDLLRQYEEBEAKAELOALSKANSEVAQWFTKYETDAIORTTELEE 328
QY 138 QMKYLEQOODETQAOEAGRLRSKMTMEQIELLSQSLPEVEEMIRDMGVGSAVEQL 197
Db 329 AKKTLAQRLQE--AEQVEAVNSKCSLEKTKRQLQA---EVEDLWVDVERSSAAAL 382
QY 198 -----AVYCVSLKKEYEN-----LKEARAKAGEV-----ADKLR----- 226
Db 383 DKORNFQVLAEWKQKQYEEAQAELESALKDARMSSTEIFMKNAVEESLDQLETLKRN 442
QY 227 -----KDLFSSRSKLTQYVSELDOAKLELSAQKDLQADKEITSLKKLTLMQET 277
Db 443 KNLQOETSDLTQETSEGTQYHELEKAKKLVQEKSDQLQALEAEAGLESKESTLRQ 502
QY 278 LNPVASETVDRVLVLESPAPVEVNLKRRPSFRDIDLNTAFDVL-----TPPARPSSSQ 333
Db 503 LELNQKSE--VDRKIAKDEITE--QLKRNRSKRIIDTMQSTLSEIRSDALRLKKKM 558
QY 334 HGYLEKLCLEKSHSPIQ--DVPKRI--CKGRKESQSLGQSCAGPEDEELVCAFPITV 389
Db 559 EGDINLELEIQLSHANRQAAEAQKOLRVNQAHLKDNQLQDLD--ALRSQEDLKEQVAVVE 615
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QY 390 RNALIGOKOPKRRPS--ESSCSKDVVRITGFDGLGRTFKFIQPTDITVI 435
Db 616 RRNNLQOAEIETIRSALEOTERSKRYABQELDASERVLQHSQNTSLI 664

RESULT 26
Q99MT2 PRELIMINARY; PRT: 976 AA.
AC Q99MT2;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE RAB6-INTERACTING PROTEIN 2 ISOFORM A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Monter S., Janoueix-Lerosey I., Jollivet F., Goud B.;
RT "Characterization of a novel interaction partner of the small GTPase
RT Rab6.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF340028; AAK26381.1; -
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR000533; TROPOMYOSIN.
DR PRINTS: PR00194; TROPOMYOSIN.
SQ SEQUENCE 976 AA; 111931 MW; 48731867C8D8C6F CRC64;

Query Match 7.4%; Score 176.5; DB 11; Length 976;
Best Local Similarity 20.5%; Pred. No. 0.063;
Matches 84; Conservative 77; Mismatches 137; Indels 111; Gaps 14;

QY 8 TICSDFPHSRDVAALHCGHTFHLQCLIQSFETAPRTCPQCRIOVG-----KRTII 59
Db 491 TLNFQFSDSKQ-----HIEVLKESL--TAKEGRAAILQTEVDALRLRLEKETML 538
QY 60 N---KLEFDLAQE-----ENVLDRE-----FLKNELDNVRAQLSQKDKKRSQ 101
Db 539 NKRTKOIQDMAEEKGTOAGEIHDKLMDLVKERVNVLAQKIKINLEQLKREKQMSLK 598
QY 102 VIIDTLRDLTEERNATVVSLOALGKAEMLCSTLKQKMYLEQOODETQAOEAGRLRS 161
Db 599 ERKSLQADPTNTDITLTTEBALADKERTIERLK-----EQDRDERKQEEIDITPK 652
QY 162 KMKTMEQIELLSQSLPEVEEMIRDMGVGQS-----AVEQLAVYCV- 202
Db 653 DLKDLREKVSILQGDISEKEASLIDIKEHASLSLASSGLKKDSRLKLTLELQEKKECK 712
QY 203 ----SLKKEYENLKEARAKAGEVADK--LRKDLFSSRSKLTQYVSELDOAKLELSAQKD 256
Db 713 MESQLKHAHEATLEAR--ASPMSBDRIOLEIREISRYKDESSKAQTEVDRLLEIKLEVE 771
QY 257 LQSDAKREIMSL-----KKRLTLMQETLNPVASETVDR 290
Db 772 KNDKDKKIAIELESITSQYVDQKKNVANKLHKQEVEKKSAQMLKEARRRREDSLSQSQ 831
QY 291 LVLESPAPVEVNLKRRPSFRDIDLNTAFDVLTPPARPSSSQGHYEEK 339
Db 832 LQVE-----ELLMAMEK-----VKQELSEMKAKLSSTQOSLAEK 865
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RESULT 27
Q28714 PRELIMINARY; PRT: 1156 AA.
AC Q28714;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE CHROMOSOME SEGREGATION PROTEIN (SKC1).
GN AFI558.
OS Archaeoglobus fulgidus.
```


SO SEQUENCE 2473 AA; 281903 MW; 504E91A1A150A3E5 CRC64;

Query Match 7.4%; Score 175.5; DB 11; Length 2473;

Best Local Similarity 23.1%; Pred. No. 0.2; Matches 64; Conservative 63; Mismatches 105; Indels 45; Gaps 6;

QY 65 DLAGEEN---VLDREFLNELDNVRAQLSQDKERKDSQVITDRLDTEERNATVVS 120
 DB 1638 ELERSEENQELALIDENMLKAQVEFTLKAQKDEMTKSLRIFELDLVTYTERENLAKQOE 1697
 QY 121 LQALAGKAEMLCSTLKAKMKYLEOQ-----ODETKQAGEBGRLSKTKT 165
 DB 1698 KQSRVSELDERCSSLRLLEEKEQARVOMEDSKSAMLMLQMLKLEEEVAALCNDQET 1757
 QY 166 MEQELLQSQLPVEYEMIRMGVGSQAVEQLAVYCVSLKREYENLKEARKASGEVADKL 225
 DB 1758 LKAGQSLDQGEVYHNL-----KSSIRKLKHAIDDEKKNHILEQLKESKHADLL 1810
 QY 226 R-----KDLF---SSRSKLQTVYSELQAKLELSAQKQDSADKEIMSL 267
 DB 1811 KDRVENLEQELLSEKKNMIFQAEKSKAEIQTLKSEIQMAQNLODLQLELSTRESENEL 1870
 QY 268 KKKLTMLQETLNLPPVASETVDRVLVLESPAVEVNLK 304
 DB 1871 IKELKEQERVSDETITNPISIELN-LKDKQEKVQMK 1906

RESULT 32

044929 PRELIMINARY; PRT; 1690 AA.

AC 044929;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE MICROVIBRIE BINDING PROTEIN D-CLIP-190.
 GN CLIP-190 OR CG5020.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON R;
 RC Lantiz V.A., Miller K.G.;
 RL J. Cell Biol. 0:0-0(1998).
 DR EMBL: AF041382; AAB96783.1;
 DR FlyBase: FBgn0020503; CLIP-190.
 DR InterPro: IPR000938; CAP-Gly.
 DR Pfam: PF01302; CAP_GLY; 2.
 SO SEQUENCE 1690 AA; 189103 MW; BEAF48FD15F17A7C CRC64;

Query Match 7.3%; Score 175; DB 5; Length 1690;

Best Local Similarity 20.9%; Pred. No. 0.14; Matches 84; Conservative 84; Mismatches 157; Indels 76; Gaps 13;

QY 50 RIQVGRITIKLFFDLAGEEENVLDRFLKNE--LDNVRKQSQDKERKDSQVITDRL 107
 DB 724 QIQLEKESIEQL--ALKONLEDFQKKQSEVHLQETIKQONQKDELVESESLSKL 781
 QY 108 RDTLEERNATVVSLOALGKAEMLCSTLKQMK--YLEQOODETRQAOEAGRLSKMKTM 166
 DB 782 QQQLEETLIGHEKIQALV-----ELKKEKETIIEKEBELQLOQSKSSESALKVY 834
 QY 167 E-QIETLLQSQLPVEYEMIRMGVGSQAVEQLAVYCVSLKREY-----209
 DB 835 QVQLEEQLOQQAASGEGSKTVARLHDEISQLSQAEETQSEKSTESNLEAKSKOLEAA 894
 QY 210 --NKEARKASGEVAD--KLRKDLFSSRSKLQTVYSELQAKLELSAQKQDSADKEI 264
 DB 895 NGSLEEKAKSGQLOEQITTKLSEVEETQALSSYHTDVESTKQLEAANAALKEVKNKE 954

QY 265 MSLKKLTMLQETLNLPPVASETVDRVLVLESPAVEVNL--LKLRRPSFRDID----DLN 317
 DB 955 AESRAEASDLDQKY-----KEITDTLHAELOAERSSSALHTLSKFSDEIATGHKELT 1008
 QY 318 ATEPV-----DTPPARSSQHGYYEKLCLKESHSPIQDVPKKIC 357
 DB 1009 SKADAWSQEMLQKEKELEQLRQQLQDSQDSQTKLAKGERKESFEES---IKMLQEEVT 1065
 QY 358 KGPRKESQSLSGGSCAGEPDELVGAFPIFVRRAIIGOKQ 398
 DB 1066 KAKTENLELSTGTQTTIKDLOERLE-----ITNAELQHK 1100

RESULT 33

090PS1 PRELIMINARY; PRT; 529 AA.

AC 090PS1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE KIAA1081 PROTEIN (FRAGMENT).
 GN KIAA1081.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RC MEDLINE=9937452; Pubmed=10470851;
 RA Kikuno R., Nagase T., Ishikawa K., Hirosewa M., Miyajima N.,
 RA Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro."
 RL DNA Res. 6:197-205(1999).
 DR EMBL: AB029004; BAA83033.1;
 DR HSSP: P01100; IPOS.
 DR InterPro: IPR002017; Spectrin.
 FT NON_PEP
 SO SEQUENCE 529 AA; 61417 MW; 08D942A9ACC63F22 CRC64;

Query Match 7.3%; Score 174.5; DB 4; Length 529;

Best Local Similarity 20.2%; Pred. No. 0.042; Matches 86; Conservative 84; Mismatches 155; Indels 101; Gaps 15;

QY 30 HLCQLOSFETAPSRCTPCRCRIQV-----KRTIIN--KLFDLAGEE-----70
 DB 11 HIEVLKESL-TAKQORAAIILQTEVDALRLRLKEKETMLNKKTKQIQDMAEKEGTQAGEIH 69
 QY 71 --ENVLDRE---FLKNELDNVRRAQLSQDKERKDSQVITDRLDTEERNATVVSLOQ 123
 DB 70 DLKMDLVKRRKVVNLQKKILENLQEOQLRDKQSSLSKEVKSLSQADVTMTDALTTLEE 129
 QY 124 ALGKAEMLCSTLKQMKYLLQOODETRQAOEAGRLSKMKTHEQIQLLQSQLPVEYEM 183
 DB 130 ALAKKETIERLK-----EQRODEREKQEBIDNKKDKLQDKLEKYSLLQGLDSEKAS 183
 QY 184 IRMGVGS-----AVQQLAVYCV---SLKREYENLKEARKASGEV 221
 DB 184 LLDLKEHASSIASGLKQDSRLKTLFETALBQKKEECLKMSQKLKAHEALLEAR-ASPEM 242
 QY 222 ADK---LRKDLFSSRSKLQTVYSELQAKLELSAQKQDSADKEIMSL-----267
 DB 243 SDRIQHLERBITRYKQDSSKAQAEVDRLEILEVEENEKNDKQKIAELSLSTRQVKQ 302
 QY 268 -----KKLTMLQETL--NLPPVASETVDRVLVLESPAVEVNLKLRP 308
 DB 303 NKVYANLKHKEQYVEKKSAQMLEARRENLDSSQQLDLSLRKKDRILEEL-----EE 357
 QY 309 SFRDDIDLNATFDV--DTPPARSSQHGYYEKLCLKESHSPIQDVPKKICGKPR---361


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Db 358 ALRESVOITAREVAVLAQESARTNAEKOVDELLAMEKVKOELESMKAKLSTQOSLAE 417
QY 362 KESOLS 367
Db 418 KETHLT 423

RESULT 34
P87344 PRELIMINARY; PRT: 1119 AA.
ID P87344
AC P87344;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MOSIN HEAVY CHAIN (FRAGMENT).
OS Theragra chalcogramma.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidae; Gadidae;
OC Theragra.
OX NCBI_TaxID=48550;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FAST MUSCLE;
RA Togashi M., Hirayama Y., Kakinuma M., Watabe S., Ojima T., Nishita K.;
RT "cDNA cloning of Alaska pollock fast skeletal muscle myosin heavy
RT chain."
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB000214; BAA19070.1; -.
DR HSP; P13538; 2MYS.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
FT NON_TER 1
SQ SEQUENCE 1119 AA; 128626 MW; B8C5FECA665B954 CRC64;

Query Match 7.3%; Score 174.5; DB 13; Length 1119;
Best Local Similarity 23.9%; Pred. No. 0.094;
Matches 79; Conservative 63; Mismatches 115; Indels 73; Gaps 13;

QY 31 LOCIOSEFETAPSRICPOCRIOVGKRTINKLFPDLAQEENVDLREP----- 78
Db 327 LEETSERLEEGGATSAQIEMKKREAFQKLRDL---ESTLOHEHTAALKKQADS 383
QY 79 ---LKNELDNVRAQLSOKDEKRDQVLIIDRLTLEERNATVVSLOALGKAEMLCSTL 135
Db 384 VAEIGEOIDNLQRYKQKLEKSEFKMEIDLSNME-----AVSKAKGNLEKICAL 436
QY 136 KKQKYLEQOODETKQAOEAGRLSKMT-----MEQIELL-----OSQLEPV 180
Db 437 EDQLEIKAKDENARQVNDISAQRARLTNGEGRQLEKALVSQLTRGKQAYTVQV 496
QY 181 EEMTRDMGVGSAVEOLA-----VYCVSLKKEYENKEAR-----KASGVADKL 225
Db 497 EELKRONEEVAKKNAALAHGVOSARHCDLREPFEEQEKAEIQRGMSANGEVA--- 553
QY 226 RKDLFFSRSKLQTF---VYSELDAQLELKSQKDLQSAKDEIKSLKMLTMOLETLNP 281
Db 554 -----QMSKRYETDAIQRTLEESKKKL--AQR--LQEAEPQIEAVNSKCSLETKQ-- 603
QY 282 PVASTVDRLY--LESPAVENVNKLRRPSF 310
Db 604 RLQGEVEDLWVDERANGLANLDKKQKNF 633

RESULT 35
Q9YHD4 PRELIMINARY; PRT: 671 AA.
ID Q9YHD4
AC Q9YHD4;
DT 01-MAY-1999 (Tremblrel. 10, Created)
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DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MOSIN HEAVY CHAIN (FRAGMENT).
GN MHC-5.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TAIL MUSCLE, HINDLIMB MUSCLE;
RA Hu H., Merrifield P., Atkinson B.G.;
RT "Expression of the Myosin Heavy Chain Genes in the Tail Muscle of
RT Thyroid Hormone-induced Metamorphosing Rana catesbeiana Tadpoles."
RL Dev. Genet. 0:0-0(1999).
DR EMBL; AF097908; AAD13773.1; -.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
FT NON_TER 1
SQ SEQUENCE 671 AA; 78062 MW; 1904A262790CA26F CRC64;

Query Match 7.3%; Score 174; DB 13; Length 671;
Best Local Similarity 21.9%; Pred. No. 0.058;
Matches 106; Conservative 92; Mismatches 167; Indels 118; Gaps 20;

QY 68 QEEENVLD-----REFLKNELDNVRAQLSOKDEK-----RDSQVLIIDRLTLEERN 115
Db 30 EKSLSQSQRQAPATQOEELKRLQLEETKAKNLAHALQSAHRCDDLRFQYEEDQ 89
QY 116 ATVVSLOALGKAMLS-----TLKKOMKYLEQOODETKQAOEAGRLR 160
Db 90 EAKAELQRLSKANSEVSWRTKYETDAIQRTLEELKAKKLAQRLQE--AEQIEAVN 146
QY 161 SKMKTMOIELLQSQLPEVEEMTRDMGVGSAVEOLAAYCVSLKKEYENL----- 211
Db 147 SKCASLETKORLQD--EVEDLWVDERNSA-----CTALDKKQKNFYKLSWMQ 196
QY 212 -----KEARKASGEVADKLKLDLFFSRSKLQTV----- 239
Db 197 KYEEQAELQAEKQESRSLSTEVE--KKNNYEALDQLETLKRNKNLQOESLDTQVA 255
QY 240 -----YSELDAQLELKSQKDLQSAKDEIN--SLK--KKLTMQLETLNPVASTVDRLY 292
Db 256 ESGKSIHEIEKAKQVEQEKSELQSALEAEGSLHEEAKILRVQLEINQKSE--VDRKY 314
QY 293 LESPAPVENVNKLRRPSRDDIDLNATPFVDV---TPPARSSSQHGVEKLCLEKSHSP 348
Db 315 AEKDEEIE--QLKRNQSALESQTSLSQSEVSRNDALRLKKKMEGLNMEQLSHAN 371
QY 349 IQ--DVPRKI--CGPRKESQSLGQSCAGEPDELVGAPIFVNAIIGOKOPKRP 404
Db 372 RQAABQQLLNQVQGFQDAQLHLD--AIRGNLDKEQLAIYERRNNLMQAEIEEMRS 428
QY 405 ---ESSCSKDVVRIGFDLGRFTFIQPTDTVMIRPLPVKAKRTYVKQVRKYTVPSLFOA 461
Db 429 ALQETERRKVAHEHLLDVTVERVOLHTQNTSLI-----NFKKLEADV---SOFOS 477
QY 462 KLD 464
Db 478 EVD 480

RESULT 36
Q98TQ5 PRELIMINARY; PRT: 975 AA.
ID Q98TQ5
AC Q98TQ5;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
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DE MYOSIN HEAVY CHAIN (FRAGMENT).
GN MYOHC-A3 GENE.
OS Notothenia coriiceps (black rockcod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Notoleosteoi;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes;
OC Notothenioidae; Nototheniidae; Notothenia.
OX NCBI_taxid=8208;
RN [1]
RP SEQUENCE FROM N.A.
RA Gavry L., Ettalaie C., Goldpink G.;
RT "Characterisation of red and white muscle myosin heavy chain gene
RT coding sequences from Antarctic and tropical fish.";
RL Comp. Biochem. Physiol. 127:575-588(2000).
DR EMBL; AJ243768; CAC27777.1; -.
DR HSSP; P03437; IHTM.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR NON_TER 1
SO SEQUENCE 975 AA; 112313 MW; 2F7AD46A3419537F CRC64;

Query Match 7.3%; Score 173.5; DB 13; Length 975;
Best Local Similarity 22.1%, Pred. No. 0.092;
Matches 72; Conservative 67; Mismatches 122; Indels 65; Gaps 11;

QY 31 LQCLQSETAPSRCPGCRIOVGKRTTIINKLFPDLAEEENVLDREF----- 78
D 183 LEEISERLEEAGATSAQIEKKKREAEFOKLRDL---EESTLOHEHTASALRKQADS 239
QY 79 ---LKNELDNVRAQLSQDKRDSQVIITLRTLEERNATVYSLQALKAEMLCSTL 135
D 240 VAELEQIDNQLQKQKLEKESEYKMEIDLISSNME-----NVAKAKNLEKWCRTL 292
QY 136 KKQMYLEQOODE-----TKQAEAGRL---RSKMTMEOI 169
D 293 EDQFSELTKNDENVROINDTSSQKARLITENGERSQVEEKEALVSLTGKQASTQOI 352
QY 170 ELLIQLQSLPEYEMIRDMGVQSAVEQLAVYCVSLKKEYENLKEKRAKSGEYADKLKRD 229
D 353 DELKR---QIEEYKAKNALAHGQSAHRHDCDLREQFEEOEKAKELQKMSANSEV 408
QY 230 FSSRSKLTQ---VYSELQAKLELSAQKDLQASDKETMSLKKTLTLOETLNLPPVAS 285
D 409 AQMSKVTYTDALQRTTEELSESKKL--AQR-LQEAHQIEAVNSGASLEKTKQ--RLQS 463
QY 286 ETVDRLV-LESPAPYEVNLLKLRPSF 310
D 464 EVEDIMIDVERANALANLDRKQRF 489

RESULT 37
096063 PRELIMINARY; PRT; 1743 AA.
AC 096063;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN (FRAGMENT).
GN DUMHC-B.
OS Dugesia japonica (Planarian).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Dugesia.
OX NCBI_taxid=6161;
RN [1]
RP SEQUENCE FROM N.A.
RA Kobatashi C., Agata K., Orli H.;
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
DE SEQUENCE FROM N.A.
RA Kobayashi C., Kobayashi S., Orli H., Agata K., Watanabe K.;

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RT "Identification of two distinct muscles in the planarian, Dugesia
RT japonica, by the expression of myosin heavy chain genes.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: BELONGS TO THE GTR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; AB015485; BAA34955.1; -.
DR HSSP; P08799; IAMD.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR001637; Glna_adenyltn.
DR InterPro; IPR000524; HTH_GntR.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001609; myosin_head.
DR InterPro; IPR002928; myosin_tail.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00612; IQ; 2.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00035; HTHGNT.
DR PRINTS; PR00193; MYOSINHEAVY.
DR PRINTS; PR00194; TROPOMYOSIN.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00182; Glna_ADENYLATION; UNKNOWN_1.
DR PROSITE; PS00096; IQ; 1.
KW DNA-binding; Transcription regulation.
FT NON_TER 1
SO SEQUENCE 1743 AA; 200417 MW; 0D4A821FA6CF7C2 CRC64;

Query Match 7.3%; Score 173.5; DB 5; Length 1743;
Best Local Similarity 22.6%, Pred. No. 0.17;
Matches 94; Conservative 75; Mismatches 160; Indels 87; Gaps 16;

QY 51 IQVGKRTTIINKLFPDLAEEENVLDREFLKNELDNVRAQLSQDKER-----RDSQVI 103
D 839 VEKAKR---KVEGELKQNDLMDLEKSELSE---QLKRRKMEIANGANSKLTEDENNL 891
QY 104 IDTLRTLEERNATVYSLQ-----QALGKAEMLCSTLKQMYLYQOODE---TQAO 153
D 892 VATLQRIKLEIQLARIQLEEDLEAERQARAERAKHQLEAIEVEERLEEQAGATQAO 951
QY 154 EAGRLRS---KMK-----TMEQIELLOS-----QLPEVE---EMIRD 186
D 952 TDLAKKRBAELMLKLRQLEENMGMHQAINGTRKKQODTANEFADQDLQKSKTIERE 1011
QY 187 MGVQSAVEQLAVYCVSLKKEYENLKEKRAKSGEYADKLKRDLFSSRSKLTQYVSELQQA 246
D 1012 KNEIRGDIEDLSGOLESINKAKIMLEKSNKGLFATISLQNKRLDELTKQLSDAGNSNNRN 1071
QY 247 KLELSAQKDLQASDKETMSLKKTLTLOETLNLPPVASEYVDVLYLESPAPYEVNLLKLR 306
D 1072 QHENSELKSLEDAESQINQSLKAKQDLQAL-----EEAKQNLDESESRKSKLTNDLR 1125
QY 307 RPSFRDDIDLNATPDVDTPPARPSSOHGYEKLEKSHSPIQDVPPKTKCKGPKRESQL 366
D 1126 -----NALSDDLA--MRES-----LEEDEGKSDVGRQLYKQVNEIQL 1162
QY 367 SLGQSCAGEPEDELVGAFLFVR--NALIGQKPKRPRESSCSK--DYVRTGFDG 419
D 1163 KNSQGTGVVSEEM-----EEFKRKMNARIQLEEESESNKSKSQLEKVSRLQG 1214

RESULT 38
09AMC4 PRELIMINARY; PRT; 437 AA.
AC 09AMC4;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE M18 PROTEIN.
GN EMM18.2.

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OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxId=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Eschaki M., Manaf A., Yusoff K., Jamal F.;
 RT "Sequence Analysis of the 5' Region of the emm Gene of Group A
 RT Streptococci Isolates from Malaysia."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF326566; AKK11617.1; -
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR InterPro: IPR003345; M_repeat.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF02370; M; 9; Gram_pos_anchor; 1.
 DR PRINTS: PRO0015; GPOSANCHOR.
 DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
 KW Transmembrane.
 SQ SEQUENCE 437 AA; 48849 MW; F1D1F586567EDDB CRC64;

Query Match 7.3%; Score 173; DB 2; Length 437;
 Best Local Similarity 22.9%; Pred. No. 0.041;
 Matches 77; Conservative 67; Mismatches 140; Indels 52; Gaps 11;

OY 66 LAQEEENVLDREFL---KNE-----LDNVAQLSOKKEDRDSOVIIDFLRD 109
 DB 105 LATOKEN-LEKEVVEAKHKHETLININDLTCLKINETROELANKQDSKENE---KTLNE 160
 OY 110 TLEERNATVVSLOALGKAEMLCSTLKKOMKYLEQOODETKQAOE-----EAGRLRSKM 163
 DB 161 LLEETVAKDKIAREQ---KSKQDFGLNQELAKKEQNKISDASRKGRLRDLDASREAKKQ 217
 OY 164 KTMEOIELLLOSQLEPEVE--MIRDAGVGSAYBQLAVYCVSLKEVENLKEAKKAGEV 221
 DB 218 LEAEHQLEBQNKISEASRRGLRDIDASREAKQVEKDLANLTAELDKYKEEQISDAS 277
 OY 222 ADKLKRDLFSSRSKLTQVYSELDOAKLELKSQAQDLQADKEIMSKKLTMLQETLNP 281
 DB 278 RQGLSRLEASREYKKEVADLAANSKLSPLKSLKLVKNYKK-KLLSSRRLE 336
 OY 282 PVASETVDRVLVLESPAVEYNLKLRRPSFRDDIDLNATFVDPAPPARSSOHGYEKLK 341
 DB 337 AEAKALKEQLAKQA---EELAKLR-----AGKASDSQFPAKPGN-----KVV 376
 OY 342 LEKSHSPIQDVPPKTKICGPKRKESQLSGGOSGAGEP 377
 DB 377 PGKQAPQAGCTKPNONKAPMKETKRQLPSTGGEANP 412

RESULT 39
 O99MI1 PRELIMINARY; PRT; 1120 AA.
 AC O99MI1;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE RAB6-INTERACTING PROTEIN 2 ISOFORM B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Monter S., Janoueix-Lerosey I., Jollivet F., Goud B.;
 RT "Characterization of a novel interaction partner of the small GTPase
 RT Rab6."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF340029; AAK26382.1; -
 DR InterPro: IPR002017; Spectrin.
 SQ SEQUENCE 1120 AA; 128330 MW; A542B526FAEDF9C7 CRC64;

Query Match 7.3%; Score 173; DB 11; Length 1120;
 Best Local Similarity 19.6%; Pred. No. 0.11;
 Matches 87; Conservative 88; Mismatches 165; Indels 104; Gaps 15;

OY 8 TICSDFPHSRDVAIAHCHFHLCLOISFETAPSRTPCQRIQV-----KRTII 59
 DB 491 TLTNQFSDSKQ-----HIEVLKESL-TAKEDRAAILQTEVDALRLREKETML 538
 OY 60 N---KLFEDLAQAE-----ENVLDRE-----FLKHELDNVAQLSOKKEDRDSO 101
 DB 539 NKTKTKQIDMAEKGQAGEIHDLKMDLVKERRVNVYLOEKIENLQELDKERKQMSL 598
 OY 102 VIIDTLRDTLEERNATVVSLOALGKAEMLCSTLKKOMKYLEQOODETKQAOEAGRLRS 161
 DB 599 ERKKSILQADQNTNDYALTLTEALADKERIERLK-----EQRDRERKQGEIITYKK 652
 OY 162 KMTMEQIELLLOSQLEPEVEEMIRMGVGS-----AVEQLAVYCV- 202
 DB 653 DLKDLREKVALLOGDSEKESASLDIKENHASSLASSGLKKDSRLKTLLEALQKKECLK 712
 OY 203 ---SLKKEYNLKEARKAGEVADK---LKDLFSSRSKLTQVYSELDOAKKLEKSAQKD 256
 DB 713 MESQLKHAHATLEAR-ASPEMSDRIQLEIREISRYKDESSKAQTEVDRLLEIKVEENE 771
 OY 257 LQSADEKIMSL-----KKKLTMLQETLNPVASETVDR 290
 DB 772 KNDKDKKIALLESITSQVQNDQKKYANLKHKEQVEKKSAQMLEKRRRDESLSDSSQ 831
 OY 291 LVLESPAVEYNLKLRRPSFRDDIDLNATFVDP---DTPARPSSOHGYEKLKESHS 347
 DB 832 L-ODSLRKDDRIELELEALRESQVLAERENVLAQESARTNAKQVEELLMAEKVKQ 890
 OY 348 PIQDVPPKTKICPR---KESQLS 367
 DB 891 ELESMAKLSLSTQOSLAKEKETHLT 914

RESULT 40
 O9YHD7 PRELIMINARY; PRT; 708 AA.
 AC O9YHD7;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN (FRAGMENT).
 GN MHC-2.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxId=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TAIL MUSCLE; HINDLIMB MUSCLE;
 RA Hu H., Merrifield P., Atkinson B.G.;
 RT "Expression of the Myosin Heavy Chain Genes in the Tail Muscle of
 RT Thyroid Hormone-Induced Metamorphosing Rana catesbeiana Tadpoles."
 RL Dev. Genet. 0:0-0(1999).
 DR EMBL: AF097905; AAD13770.1; -
 DR InterPro: IPR002928; Myosin_tail.
 DR InterPro: IPR000533; Tropomyosin.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS: PRO0194; TROPOMYOSIN.
 FT NON_TER 1
 SQ SEQUENCE 708 AA; 81824 MW; BE2D017000179C4C CRC64;

Query Match 7.2%; Score 172.5; DB 13; Length 708;
 Best Local Similarity 22.7%; Pred. No. 0.074;
 Matches 93; Conservative 83; Mismatches 142; Indels 91; Gaps 19;

OY 45 TPCQRIQVGKRTIINKLFEDLAQEEENVLD-----REFKNELDNVAQLSOKKEDK-- 97
 DB 47 TTQARARLQTEGELSRL-----EKEKSLISQLSRGKIGFTQGVLEIKRLQLEESKAKNA 101

